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22. (Amended) The method of claim 36, wherein the aligning is performed by an algorithm selected from the group consisting of a Smith-Waterman algorithm, Needleman-Wunsch algorithm, a BLAST algorithm, a FASTA algorithm, and a PSI-BLAST algorithm.

23. (Amended) The method of claim 36, wherein at least one polypeptide sequence is obtained by translating a nucleic acid sequence from a genome database.

B5 24. (Amended) The method of claim 36, wherein the sequences are from a database.

25. (Amended) The method of claim 36, wherein at least the first protein has a known function.

26. (Amended) The method of claim 36, wherein at least one of the proteins has an unknown function.

27. (Amended) The method of claim 36, wherein the alignment is based on the degree of homology of the nucleic acid or polypeptide sequences of the first and second proteins to a segment of the nucleic acid or polypeptide sequence of the third protein.

28. (Amended) The method of claim 36, further comprising determining the significance of the aligned and identified second nucleic acid or polypeptide by computing a probability (p) value threshold.

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B6 30. (Amended) The method of claim 36, further comprising filtering excessive functional links between the first protein and any second protein.

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B7 34. (Amended) A method for identifying a second nucleic acid sequence or second polypeptide sequence of a second protein, wherein the second protein has a biological or chemical property of interest, comprising:

(a) providing a first nucleic acid sequence or a first polypeptide sequence comprising the biological or chemical property of interest;

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CDU+  
(b) providing at least one algorithm capable of analyzing a functional relationship between the first protein and second protein selected from the group consisting of a "domain fusion" method, a "phylogenetic profile" method, and a "physiologic linkage" method; and

(c) comparing the first nucleic acid sequence or the first polypeptide sequence to a plurality of sequences using at least one of the algorithms as set forth in step (b) to identify the second nucleic acid sequence or second polypeptide sequence of the second protein which has a functional relationship to the first protein, thereby identifying a nucleic acid sequence or polypeptide sequence of a protein that possesses the property of interest. --

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Please add new claims:

-- 35. (New) The method of claim 35, wherein the property of interest is a binding or catalytic site or cellular localization.

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36. (New) The method of claim 1 or 2, wherein the "domain fusion" method comprises:

(a) providing a pair of non-homologous nucleic acid or polypeptide sequences of the first and second proteins, respectively;

(b) providing a third nucleic acid or polypeptide sequence of a third protein;

(c) aligning the sequences of the first and second proteins in step (a) to a segment of the sequence in step (b); and

(d) establishing whether a significant sequence similarity is present between the alignments of step (c),

wherein identification of a significant sequence similarity between the sequences of the first and third protein and the second and third protein identifies the first and second proteins as having a functional relationship.

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